Abstract

Bovine papillomaviruses (BPV) are small nonenveloped dsDNA viruses belong to the family *Papillomaviridae*. One of the characters of this family is strong species and tissue specificity, but some BPVs are represent an exception and they are able to infecting other groups of vertebrates. However transmission on human has not been proved yet. All viruses from this groups, including BPV have considerable tumorigenic potential, in particular for the infection non-permissive cells. In the natural host, they are causing clinical disease, which manifest papillomas, that may interfere with host of life what cause considerable economic loss. BPV served as model organisms for study. Papillomavirus family and these findings helps understand their human counterparts (human papillomaviruses, HPV). Recently, studies of BPV are not so frequent, overshadowed the success of vaccines against HPV. To the other hand, this success is encouradged for as to develop the similar vaccines against BPV order to avoid disease of farm animals. The successful development working on such a vaccine, is needed understand function virus and viral proteins and mechanism their interaction with the host cell. It is also necessary to map individual BPV their similarites and differences that to the specifics of each types. This work present such an overview.

Keywords: bovine papillomavirus, disease, viral protein, capsid, genome